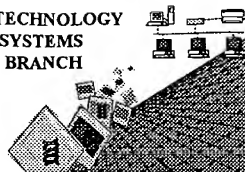# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/943,944_
Source: _OIPE,_
Date Processed by STIC: _1/31/2002_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
 PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
 PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
        http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. **Hand Carry directly to:**
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
                Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: 09/943,944 |

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ___ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ___ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ___ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ___ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ___ Variable Length

Sequence(s) ___ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ___ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) ___. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ___ Skipped Sequences
(OLD RULES)

Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ___ Skipped Sequences
(NEW RULES)

Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ___ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10 ___ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220><223> section is required when <213> response is Unknown or is Artificial Sequence

11 ___ Use of <220>

Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ___ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ___ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

```
RAW SEQUENCE LISTING              DATE: 01/31/2002
PATENT APPLICATION:  US/09/943,944   TIME: 12:56:30

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\01312002\I943944.raw
```

Does Not Comply
Corrected Diskette Needed

pp 2-6

```
              SEQUENCE LISTING
 4 (1) GENERAL INFORMATION:
 6      (i) APPLICANT: Ptashne, Mark
 7                     Xiangyang, Lu
 8                     Yibing, Wu
10     (ii) TITLE OF INVENTION: Transcriptional Activation System,
11                             Activators, and Uses Therefor
13    (iii) NUMBER OF SEQUENCES: 238   a (use/lower-case letter)
15     (iv) CORRESPONDENCE ADDRESS:  a
16          (A) ADDRESSEE: Choate, Hall & Stewart
17          (B) STREET: 53 State Street
18          (C) CITY: Boston
19          (D) STATE: MA
20          (E) COUNTRY: USA
21          (F) ZIP: 02109
23      (v) COMPUTER READABLE FORM:
24          (A) MEDIUM TYPE: Floppy disk
25          (B) COMPUTER: IBM PC compatible
26          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
29     (vi) CURRENT APPLICATION DATA:
C--> 30          (A) APPLICATION NUMBER: US/09/943,944
C--> 31          (B) FILING DATE: 07-Jan-2002
32          (C) CLASSIFICATION:
34    (viii) ATTORNEY/AGENT INFORMATION:
35          (A) NAME: Jarrell Ph.D., Brenda H
36          (B) REGISTRATION NUMBER: 39,223
37          (C) REFERENCE/DOCKET NUMBER: 0342941-0065
39     (ix) TELECOMMUNICATION INFORMATION:
40          (A) TELEPHONE: 617 248 5000
41          (B) TELEFAX: 617 248 4000


ERRORED SEQUENCES

65 (2) INFORMATION FOR SEQ ID NO: 2:
67      (i) SEQUENCE CHARACTERISTICS:       P.2
68          (A) LENGTH: 18 base pairs
69          (B) TYPE: nucleic acid
70          (C) STRANDEDNESS: not relevant
71          (D) TOPOLOGY: not relevant
73     (ii) MOLECULE TYPE: DNA (genomic)
75     (vi) ORIGINAL SOURCE:
```

RAW SEQUENCE LISTING   DATE: 01/31/2002
PATENT APPLICATION: US/09/943,944   TIME: 12:56:30

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\01312002\I943944.raw

```
        76        (C) INDIVIDUAL ISOLATE: LS1 DNA sequence
        80      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
E--> 82 CCCCTCTTNN CNNCCCTC        18 (global format error - see item 1 on Error summary sheet)
W--> 83 18
        85 (2) INFORMATION FOR SEQ ID NO: 3:
        87      (i) SEQUENCE CHARACTERISTICS:
        88          (A) LENGTH: 18 base pairs
        89          (B) TYPE: nucleic acid
        90          (C) STRANDEDNESS: not relevant
W--> 91          (D) TOPOLOGY: not relevant
        93      (ii) MOLECULE TYPE: DNA (genomic)
        96     (vii) IMMEDIATE SOURCE:
        97          (B) CLONE: LS2 DNA sequence
       101      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:        same error
E--> 103 ATTCCGCCAC CGTATTTC
W--> 104 18
       127 (2) INFORMATION FOR SEQ ID NO: 5:
       129      (i) SEQUENCE CHARACTERISTICS:
       130          (A) LENGTH: 18 base pairs
       131          (B) TYPE: nucleic acid
       132          (C) STRANDEDNESS: not relevant
W--> 133          (D) TOPOLOGY: not relevant
       135      (ii) MOLECULE TYPE: DNA (genomic)
       138     (vii) IMMEDIATE SOURCE:
       139          (B) CLONE: LS3 DNA sequence
       143      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:        same
E--> 145 CTGCCCGGGT GTTTCTTC
W--> 146 18
       169 (2) INFORMATION FOR SEQ ID NO: 7:
       171      (i) SEQUENCE CHARACTERISTICS:
       172          (A) LENGTH: 18 base pairs
       173          (B) TYPE: nucleic acid
       174          (C) STRANDEDNESS: not relevant
W--> 175          (D) TOPOLOGY: not relevant
       177      (ii) MOLECULE TYPE: DNA (genomic)
       180     (vii) IMMEDIATE SOURCE:
       181          (B) CLONE: LS4 DNA sequence
       185      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
E--> 187 CAGCTCCCCC CCTGGTTA        same
W--> 188 18
       211 (2) INFORMATION FOR SEQ ID NO: 9:
       213      (i) SEQUENCE CHARACTERISTICS:
       214          (A) LENGTH: 18 base pairs
       215          (B) TYPE: nucleic acid
       216          (C) STRANDEDNESS: not relevant
W--> 217          (D) TOPOLOGY: not relevant
       219      (ii) MOLECULE TYPE: DNA (genomic)
       222     (vii) IMMEDIATE SOURCE:
       223          (B) CLONE: LS5 DNA SEQUENCE
```

```
                  RAW SEQUENCE LISTING              DATE: 01/31/2002
                  PATENT APPLICATION:  US/09/943,944   TIME: 12:56:30

                  Input Set : A:\PTO.VSK.txt
                  Output Set: N:\CRF3\01312002\I943944.raw

      227      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:      same
E--> 229 TACTGGCCCT CCCCCTTC
W--> 230 18
      253 (2) INFORMATION FOR SEQ ID NO: 11:
      255      (i) SEQUENCE CHARACTERISTICS:
      256          (A) LENGTH: 18 base pairs
      257          (B) TYPE: nucleic acid
      258          (C) STRANDEDNESS: not relevant
W--> 259          (D) TOPOLOGY: not relevant
      261     (ii) MOLECULE TYPE: DNA (genomic)
      264    (vii) IMMEDIATE SOURCE:
      265          (B) CLONE: LS6 DNA SEQUENCE
      269     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:      same
E--> 271 GAGTTCCCCT ATGACTTG
W--> 272 18
      295 (2) INFORMATION FOR SEQ ID NO: 13:
      297      (i) SEQUENCE CHARACTERISTICS:
      298          (A) LENGTH: 18 base pairs
      299          (B) TYPE: nucleic acid
      300          (C) STRANDEDNESS: not relevant
W--> 301          (D) TOPOLOGY: not relevant
      303     (ii) MOLECULE TYPE: DNA (genomic)
      306    (vii) IMMEDIATE SOURCE:
      307          (B) CLONE: LS7 DNA SEQUENCE
      311     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:      same
E--> 313 ACCGCCGAAT TCCCCCTC
W--> 314 18
      337 (2) INFORMATION FOR SEQ ID NO: 15:
      339      (i) SEQUENCE CHARACTERISTICS:
      340          (A) LENGTH: 18 base pairs
      341          (B) TYPE: nucleic acid
      342          (C) STRANDEDNESS: not relevant
W--> 343          (D) TOPOLOGY: not relevant
      345     (ii) MOLECULE TYPE: DNA (genomic)
      348    (vii) IMMEDIATE SOURCE:
      349          (B) CLONE: LS8 DNA SEQUENCE
      353     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:      same
E--> 355 CAATTTCTAG ACGCACTT
W--> 356 18
      379 (2) INFORMATION FOR SEQ ID NO: 17:
      381      (i) SEQUENCE CHARACTERISTICS:
      382          (A) LENGTH: 18 base pairs
      383          (B) TYPE: nucleic acid
      384          (C) STRANDEDNESS: not relevant
W--> 385          (D) TOPOLOGY: not relevant
      387     (ii) MOLECULE TYPE: DNA (genomic)
      390    (vii) IMMEDIATE SOURCE:
      391          (B) CLONE: LS9 DNA sequence
      395     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
```

```
                    RAW SEQUENCE LISTING              DATE: 01/31/2002
                    PATENT APPLICATION:  US/09/943,944   TIME: 12:56:30

                    Input Set : A:\PTO.VSK.txt
                    Output Set: N:\CRF3\01312002\I943944.raw       some
E--> 397 ACATTCCCTG ACCCCTTC
W--> 398 18
     421 (2) INFORMATION FOR SEQ ID NO: 19:
     423      (i) SEQUENCE CHARACTERISTICS:
     424            (A) LENGTH: 18 base pairs
     425            (B) TYPE: nucleic acid
     426            (C) STRANDEDNESS: not relevant
W--> 427            (D) TOPOLOGY: not relevant
     429      (ii) MOLECULE TYPE: DNA (genomic)
     432     (vii) IMMEDIATE SOURCE:
     433            (B) CLONE: LS10 DNA sequence
     437      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:       some
E--> 439 ATCGGCCCAN CNCTTTTC
W--> 440 18
     442 (2) INFORMATION FOR SEQ ID NO: 20:
     444      (i) SEQUENCE CHARACTERISTICS:
     445            (A) LENGTH: 18 base pairs
     446            (B) TYPE: nucleic acid
     447            (C) STRANDEDNESS: not relevant
W--> 448            (D) TOPOLOGY: not relevant
     450      (ii) MOLECULE TYPE: DNA (genomic)
     453     (vii) IMMEDIATE SOURCE:
     454            (B) CLONE: LS11 DNA sequence
     458      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:   some
E--> 460 TTGGATTTTT CCTACGTC
W--> 461 18
     484 (2) INFORMATION FOR SEQ ID NO: 22:
     486      (i) SEQUENCE CHARACTERISTICS:
     487            (A) LENGTH: 18 base pairs
     488            (B) TYPE: nucleic acid
     489            (C) STRANDEDNESS: not relevant
W--> 490            (D) TOPOLOGY: not relevant
     492      (ii) MOLECULE TYPE: DNA (genomic)
     495     (vii) IMMEDIATE SOURCE:
     496            (B) CLONE: LS12 DNA sequence
     500      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:       some
E--> 502 CCCCCACCAC CCTGGCCC
W--> 503 18
     526 (2) INFORMATION FOR SEQ ID NO: 24:
     528      (i) SEQUENCE CHARACTERISTICS:
     529            (A) LENGTH: 18 base pairs
     530            (B) TYPE: nucleic acid
     531            (C) STRANDEDNESS: not relevant
W--> 532            (D) TOPOLOGY: not relevant
     534      (ii) MOLECULE TYPE: DNA (genomic)
     537     (vii) IMMEDIATE SOURCE:
     538            (B) CLONE: LS13 DNA sequence
     542      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:       some
E--> 544 CTCTTTGAAT GAGGAACC
```

RAW SEQUENCE LISTING   DATE: 01/31/2002
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            Input Set : A:\PTO.VSK.txt
            Output Set: N:\CRF3\01312002\I943944.raw

W--> 545 18
     568 (2) INFORMATION FOR SEQ ID NO: 26:
     570   (i) SEQUENCE CHARACTERISTICS:
     571   (A) LENGTH: 18 base pairs
     572   (B) TYPE: nucleic acid
     573   (C) STRANDEDNESS: not relevant
W--> 574   (D) TOPOLOGY: not relevant
     576   (ii) MOLECULE TYPE: DNA (genomic)
     579   (vii) IMMEDIATE SOURCE:
     580   (B) CLONE: LS14 DNA sequence
     584   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:
E--> 586 CTGCTCGACA TACCTTTC
W--> 587 18
     610 (2) INFORMATION FOR SEQ ID NO: 28:
     612   (i) SEQUENCE CHARACTERISTICS:
     613   (A) LENGTH: 18 base pairs
     614   (B) TYPE: nucleic acid
     615   (C) STRANDEDNESS: not relevant
W--> 616   (D) TOPOLOGY: not relevant
     618   (ii) MOLECULE TYPE: DNA (genomic)
     621   (vii) IMMEDIATE SOURCE:
     622   (B) CLONE: LS15 DNA SEQUENCE
     626   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:
E--> 628 CTCCCCGACG CCTTTCTC
W--> 629 18
     652 (2) INFORMATION FOR SEQ ID NO: 30:
     654   (i) SEQUENCE CHARACTERISTICS:
     655   (A) LENGTH: 18 base pairs
     656   (B) TYPE: nucleic acid
     657   (C) STRANDEDNESS: not relevant
W--> 658   (D) TOPOLOGY: not relevant
     660   (ii) MOLECULE TYPE: DNA (genomic)
     663   (vii) IMMEDIATE SOURCE:
     664   (B) CLONE: LS16 DNA SEQUENCE
     668   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:
E--> 670 CTCTTCCCCG ACCTCAAC
W--> 671 18
     694 (2) INFORMATION FOR SEQ ID NO: 32:
     696   (i) SEQUENCE CHARACTERISTICS:
     697   (A) LENGTH: 18 base pairs
     698   (B) TYPE: nucleic acid
     699   (C) STRANDEDNESS: not relevant
W--> 700   (D) TOPOLOGY: not relevant
     702   (ii) MOLECULE TYPE: DNA (genomic)
     705   (vii) IMMEDIATE SOURCE:
     706   (B) CLONE: LS17 DNA SEQUENCE
     710   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:
E--> 712 TCTTGGTTTG ATGTCGAA
W--> 713 18

```
      736 (2) INFORMATION FOR SEQ ID NO: 34:
      738      (i) SEQUENCE CHARACTERISTICS:
      739          (A) LENGTH: 18 base pairs
      740          (B) TYPE: nucleic acid
      741          (C) STRANDEDNESS: not relevant
W--> 742          (D) TOPOLOGY: not relevant
      744     (ii) MOLECULE TYPE: DNA (genomic)
      747    (vii) IMMEDIATE SOURCE:
      748          (B) CLONE: LS18 DNA SEQUENCE
      752     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:       same
E--> 754 CTTGAACCTC CGCCCTGG
W--> 755 18
      778 (2) INFORMATION FOR SEQ ID NO: 36:
      780      (i) SEQUENCE CHARACTERISTICS:
      781          (A) LENGTH: 18 base pairs
      782          (B) TYPE: nucleic acid
      783          (C) STRANDEDNESS: not relevant
W--> 784          (D) TOPOLOGY: not relevant
      786     (ii) MOLECULE TYPE: DNA (genomic)
      789    (vii) IMMEDIATE SOURCE:
      790          (B) CLONE: LS19 DNA SEQUENCE
      794     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:       same
E--> 796 CAGCTACCTG ATCTGTTC
W--> 797 18
      820 (2) INFORMATION FOR SEQ ID NO: 38:
      822      (i) SEQUENCE CHARACTERISTICS:
      823          (A) LENGTH: 18 base pairs
      824          (B) TYPE: nucleic acid
      825          (C) STRANDEDNESS: not relevant
W--> 826          (D) TOPOLOGY: not relevant
      828     (ii) MOLECULE TYPE: DNA (genomic)
      831    (vii) IMMEDIATE SOURCE:
      832          (B) CLONE: LS20 DNA SEQUENCE
      836     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:       same
E--> 838 CCTCTCCCAG ACCTCTTC
W--> 839 18
```

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

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Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\01312002\I943944.raw

```
L:30  M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31  M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:50  M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=1
L:71  M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=2
L:82  M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:2
L:83  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:91  M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=3
L:103 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:3
L:104 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:112 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=4
L:133 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=5
L:145 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:5
L:146 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:154 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=6
L:175 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=7
L:187 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:7
L:188 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:196 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=8
L:217 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=9
L:229 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:9
L:230 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:238 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=10
L:259 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=11
L:271 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:11
L:272 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:280 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=12
L:301 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=13
L:313 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:13
L:314 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:322 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=14
L:343 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=15
L:355 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:15
L:356 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:364 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=16
L:385 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=17
L:397 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:17
L:398 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:406 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=18
L:427 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=19
L:439 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:19
L:440 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:448 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=20
L:460 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:20
L:461 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:20
L:469 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=21
L:490 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=22
L:502 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:22
L:503 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22
```

VERIFICATION SUMMARY   DATE: 01/31/2002
PATENT APPLICATION: US/09/943,944   TIME: 12:56:32

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\01312002\I943944.raw

```
L:511 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=23
L:532 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=24
L:544 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:24
L:545 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:24
L:553 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=25
L:574 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=26
L:586 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:26
L:587 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:26
L:595 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=27
L:616 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=28
L:628 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:28
L:629 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:28
L:637 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=29
L:658 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=30
L:670 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:30
L:671 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:30
L:679 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=31
L:700 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=32
L:712 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:32
L:713 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32
L:721 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=33
L:742 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=34
L:754 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:34
L:755 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:34
L:763 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=35
L:784 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=36
L:796 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:36
L:797 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:36
L:805 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=37
L:826 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=38
L:838 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:38
L:839 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:38
L:847 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=39
L:868 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=40
L:880 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:40
L:881 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:40
L:889 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=41
L:901 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:41
L:902 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41
L:910 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=42
L:922 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:42
L:923 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:42
L:931 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=43
L:952 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=44
L:964 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:44
L:965 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44
L:973 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=45
L:994 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=46
L:1006 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:46
```

VERIFICATION SUMMARY   DATE: 01/31/2002
PATENT APPLICATION: US/09/943,944   TIME: 12:56:32

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\01312002\I943944.raw

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L:1007 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:46
L:1015 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=47
L:1036 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=48
L:1048 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:48
L:1049 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:48
L:1057 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=49
L:1078 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=50
L:1090 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:50
L:1091 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50
L:1132 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:52
L:1133 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52
L:1174 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:54
L:1175 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:54
L:1216 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:56
L:1217 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:56
L:1258 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:58
L:1259 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:58
L:1300 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:60
L:1301 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:60
L:1342 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:62
L:1343 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:62
L:1384 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:64
L:1385 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:64
L:1426 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:66
L:1427 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:66
L:1468 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:68
L:1469 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:68
L:1510 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:70
L:1511 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:70
L:1552 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:72
L:1553 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:72
L:1594 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:74
L:1595 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:74
L:1636 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:76
L:1637 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:76
L:1678 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:78
L:1679 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:78
L:1720 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:80
L:1721 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:80
L:1762 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:82
L:1763 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:82
L:1804 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:84
L:1805 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:84
L:1846 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:86
L:1847 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:86
L:1888 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:88
L:1889 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:88
L:1930 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:90
L:1931 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:90
```

VERIFICATION SUMMARY   DATE: 01/31/2002
PATENT APPLICATION: US/09/943,944   TIME: 12:56:32

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\01312002\I943944.raw

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L:1972 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:92
L:1973 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:92
L:2014 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:94
L:2015 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:94
L:2056 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:96
L:2057 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:96
```

STATISTICS SUMMARY   DATE: 01/31/2002
PATENT APPLICATION: US/09/943,944   TIME: 12:56:32

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\01312002\I943944.raw

Application Serial Number: US/09/943,944
Alpha or Numeric: Alpha
Application Class:
Application File Date: 01-07-2002
Art Unit: OIPE
Software Application: PatentIN1.0
Total Number of Sequences: 238
Total Nucleotides: 2235
Total Amino Acids: 828
Number of Errors: 114
Number of Warnings: 352
Number of Corrections: 0

MESSAGE SUMMARY

246 W: 238 (Invalid value of Alpha Sequence Header Field)
254 E: 114 (No. of Bases conflict)
336 W: 114 (Invalid Amino Acid Number in Coding Region)